

&lt;!--StartFragment--&gt;RESULT 3

ABA94700

SEQ ID NO: 8  
alignment

Does not encode SEQ ID NO: 9

ID ABA94700 standard; cDNA; 3197 BP.

XX

AC ABA94700;

XX

DT 23-APR-2002 (first entry)

XX

DE Human lipid metabolism molecule (LMM) cDNA (ID: 7477093CB1).

XX

KW Lipid metabolism molecule; LMM; cytostatic; nootropic; neuroprotective;  
 KW anticonvulsant; immunosuppressive; anti-inflammatory; dermatological;  
 KW cardiovascular; antiHIV; antiemetic; antiallergic; hypertensive; human;  
 KW cancer; gene therapy; protein therapy; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .3081

FT /\*tag= a

FT /product= "LMM"

XX

PN WO200204490-A2.

XX

PD 17-JAN-2002.

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PF 06-JUL-2001; 2001WO-US021432.

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PR 07-JUL-2000; 2000US-0216801P.

PR 07-JUL-2000; 2000US-0216803P.

PR 14-JUL-2000; 2000US-0218233P.

PR 21-JUL-2000; 2000US-0220046P.

PR 26-JUL-2000; 2000US-0220739P.

PR 04-AUG-2000; 2000US-0222824P.

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PA (INCY-) INCYTE GENOMICS INC.

XX

PI Tang YT, Azimzai Y, Das D, Thornton M, Lu DAM, Tribouley CM;

PI Yue H, Gandhi AR, Walia NK, Khan FA, Lu Y, Yao MG, Hafalia AJA;

PI Elliott VS, Patterson C, Lal P, Ramkumar J, Nguyen DB, Baugn MR;

XX

DR WPI; 2002-164631/21.

DR P-PSDB; ABB07497.

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PT Lipid metabolism molecules useful in diagnosing, treating or preventing  
 PT cancers, and neurological, autoimmune/inflammatory, gastrointestinal,  
 PT skin and cardiovascular disorders.

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PS Claim 5; Page 126-127; 128pp; English.

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CC The invention provides human lipid metabolism molecule (LMM) polypeptides  
 CC and polynucleotides. The LMM polypeptides can be expressed by standard  
 CC recombinant methodology. The LMM polypeptides are useful for diagnosing  
 CC or treating a condition or disease associated with the expression of LMM,  
 CC or screening for compounds that specifically bind to or modulate the  
 CC activity or expression of LMM. They are also used to generate antibodies  
 CC and assess the toxicity of test compounds. The LMM polypeptides,  
 CC modulators and antibodies are specifically useful for diagnosing,  
 CC treating or preventing cancers (e.g. adenocarcinoma, leukemia, lymphoma,  
 CC melanoma or sarcoma), neurological disorders (e.g. epilepsy, stroke,  
 CC cerebral neoplasms, Alzheimer's disease or Pick's disease), autoimmune/

CC inflammatory disorders (e.g. AIDS, Addison's disease, allergies, asthma,  
 CC or atherosclerosis), gastrointestinal disorders (e.g. dysphagia, peptide  
 CC esophagitis, gastritis, gastric carcinoma, anorexia or nausea), skin  
 CC disorders (e.g. dermatitis, eczema, or scleroderma), and cardiovascular  
 CC disorders (e.g. hypertension, arterial dissections, vascular tumours, or  
 CC thrombolysis). The present sequence represents a human LMM polynucleotide  
 CC sequence

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SQ Sequence 3197 BP; 644 A; 994 C; 951 G; 608 T; 0 U; 0 Other;

Query Match 73.2%; Score 2627.4; DB 6; Length 3197;  
 Best Local Similarity 99.0%; Pred. No. 0;  
 Matches 2663; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

Qy	8	GTCCTATCCCACTGGGACCGTCGCTGCCACTCAGCCAGAGAGCCAGCATCTTGGCAAGGG	67
Db	509	GTCCTATCCCACTGGGACCGTCGCTGCCACTCAGCCAGAGAGCCAGCATCTTGGCAAGGG	568
Qy	68	CTGGGCCTGGAGTGAAGCTGGAAGGGCTAGCATGGAGAGCCTGTCACCTGGGGGACCAAC	127
Db	569	CTGGGCCTGGAGTGAAGCTGGAAGGGCTAGCATGGAGAGCCTGTCACCTGGGGGACCAAC	628
Qy	128	TGGCCACCCTTACCA-----GGGGGAGGCCTCTACCTGCT	162
Db	629	TGGCCACCCTTACCAGGGCGCCAGTGCCAGCAGACGACAGGGGGAGGCCTCTACCTGCT	688
Qy	163	GGCAGCTCACAGTGAGGGTCCTGGAGGCGCGGAACCTGCGCTGGGCTGACCTGTTGAGTG	222
Db	689	GGCAGCTCACAGTGAGGGTCCTGGAGGCGCGGAACCTGCGCTGGGCTGACCTGTTGAGTG	748
Qy	223	AGGCCGACCCTTACGTGATCCTACAGCTGTCGACCGCACCTGGAATGAAGTTTAAGACCA	282
Db	749	AGGCCGACCCTTACGTGATCCTACAGCTGTCGACCGCACCTGGAATGAAGTTTAAGACCA	808
Qy	283	AGACGCTCACCGACACCAGTCATCCTGTGTGGAATGAGGCCTTCCGTTTCCTTATCCAAA	342
Db	809	AGACGCTCACCGACACCAGTCATCCTGTGTGGAATGAGGCCTTCCGTTTCCTTATCCAAA	868
Qy	343	GTCAGGTCAAGAATGTTCTGGAGCTTAGCATCTATGATGAGGACTCAGTCACGGAGGATG	402
Db	869	GTCAGGTCAAGAATGTTCTGGAGCTTAGCATCTATGATGAGGACTCAGTCACGGAGGATG	928
Qy	403	ACATCTGCTTCAAGGTTCTCTATGACATCTCAGAAGTCCTCCCTGGCAAGCTGCTCCGGA	462
Db	929	ACATCTGCTTCAAGGTTCTCTATGACATCTCAGAAGTCCTCCCTGGCAAGCTGCTCCGGA	988
Qy	463	AAACCTTCTCCAGAGTCCCCAGGGAGAGGAGGAGCTGGATGTGGAGTTCCTGATGGAAG	522
Db	989	AAACCTTCTCCAGAGTCCCCAGGGAGAGGAGGAGCTGGATGTGGAGTTCCTGATGGAAG	1048
Qy	523	AAACGTCAGATCGCCAGAAAACCTCATCACCAACAAAGTCATTGTGGCCCGAGAGCTGT	582
Db	1049	AAACGTCAGATCGCCAGAAAACCTCATCACCAACAAAGTCATTGTGGCCCGAGAGCTGT	1108
Qy	583	CATGCCTGGATGTGCATCTGGACAGCACAGGGAGCACCGCTGTGGTTGCAGATCAGGACA	642
Db	1109	CATGCCTGGATGTGCATCTGGACAGCACAGGGAGCACCGCTGTGGTTGCAGATCAGGACA	1168
Qy	643	AGCTGGAGCTGGAGCTGGTGCTGAAGGGTCTTATGAGGACACACAGACATCCTTCCTGG	702
Db	1169	AGCTGGAGCTGGAGCTGGTGCTGAAGGGTCTTATGAGGACACACAGACATCCTTCCTGG	1228

Qy	703	GCACAGCCTCTGCCTTCCGCTTCCACTACATGGCAGCCCTAGAGACAGAGCTGAGCGGGC	762
Db	1229	GCACAGCCTCTGCCTTCCGCTTCCACTACATGGCAGCCCTAGAGACAGAGCTGAGCGGGC	1288
Qy	763	GCCTGAGGAGCTCCAGAAGCAATGGCTGGAATGGGGACAACCTCAGCTGGGTACCTCACTG	822
Db	1289	GCCTGAGGAGCTCCAGAAGCAATGGCTGGAATGGGGACAACCTCAGCTGGGTACCTCACTG	1348
Qy	823	TGCCCCCTGAGGCCCTTGACCATTGGGAAGGAGGTGACTATGGATGTTTCTGCTCCAAATG	882
Db	1349	TGCCCCCTGAGGCCCTTGACCATTGGGAAGGAGGTGACTATGGATGTTTCTGCTCCAAATG	1408
Qy	883	CCCCAGGAGTGAGGCTGCAGCTCAAGGCAGAGGGCTGCCCTGAGGAGCTGGCCGTGCACC	942
Db	1409	CCCCAGGAGTGAGGCTGCAGCTCAAGGCAGAGGGCTGCCCTGAGGAGCTGGCCGTGCACC	1468
Qy	943	TGGGCTTCAATCTCTGTGCAGAGGAGCAGGCCTTCTGAGCAGGAGGAAGCAGGTGGTGG	1002
Db	1469	TGGGCTTCAATCTCTGTGCAGAGGAGCAGGCCTTCTGAGCAGGAGGAAGCAGGTGGTGG	1528
Qy	1003	CCAAGGCCCTGAAGCAGGCCCTGCAGCTGGACAGAGACCTGCAGGAGGATGAGGTACCCG	1062
Db	1529	CCAAGGCCCTGAAGCAGGCCCTGCAGCTGGACAGAGACCTGCAGGAGGATGAGGTACCCG	1588
Qy	1063	TTGTGGGCATCATGGCCACAGGAGGAGGTGCCCCGGGCCATGACCTCACTCTACGGCCACC	1122
Db	1589	TTGTGGGCATCATGGCCACAGGAGGAGGTGCCCCGGGCCATGACCTCACTCTACGGCCACC	1648
Qy	1123	TATTGGCCTTGCAGAAGCTGGGCCTCCTAGACTGTGTGACCTACTTCAGTGGCATCTCTG	1182
Db	1649	TATTGGCCTTGCAGAAGCTGGGCCTCCTAGACTGTGTGACCTACTTCAGTGGCATCTCTG	1708
Qy	1183	GCTCTACGTGGACAATGGCCCACCTGTACGGGGACCCTGAGTGGTCGCAGAGGGACCTGG	1242
Db	1709	GCTCTACGTGGACAATGGCCCACCTGTACGGGGACCCTGAGTGGTCGCAGAGGGACCTGG	1768
Qy	1243	AGGGACCTATCAGATACGCCGGGAGCACCTGGCCAAGAGCAAGCTGGAGGTCTTTTCCC	1302
Db	1769	AGGGACCTATCAGATACGCCGGGAGCACCTGGCCAAGAGCAAGCTGGAGGTCTTTTCCC	1828
Qy	1303	CAGAGCGCCTGGCGAGCTACCGCCGGGAGCTGGAGCTGCGGGCTGAGCAGGGCCACCCCA	1362
Db	1829	CAGAGCGCCTGGCGAGCTACCGCCGGGAGCTGGAGCTGCGGGCTGAGCAGGGCCACCCCA	1888
Qy	1363	CGACCTTTGTGGACCTGTGGGCGCTAGTGCTGGAGTCCATGCTGCACGGCCAGGTGATGG	1422
Db	1889	CGACCTTTGTGGACCTGTGGGCGCTAGTGCTGGAGTCCATGCTGCACGGCCAGGTGATGG	1948
Qy	1423	ATCAGAAGCTGTCAGGACAGAGAGCCGCCCTGGAACGGGGTCAGAACCCTCTGCCCCCTCT	1482
Db	1949	ATCAGAAGCTGTCAGGACAGAGAGCCGCCCTGGAACGGGGTCAGAACCCTCTGCCCCCTCT	2008
Qy	1483	ACTTGAGCCTCAATGTCAAAGAGAACAATCTGGAGACACTGGACTTCAAGGAGTGGGTTG	1542
Db	2009	ACTTGAGCCTCAATGTCAAAGAGAACAATCTGGAGACACTGGACTTCAAGGAGTGGGTTG	2068
Qy	1543	AGTTCTCCCCCTATGAGGTCGGTTTCTTGAAGTACGGGGCCTTCGTCCCTCCTGAGCTCT	1602
Db	2069	AGTTCTCCCCCTATGAGGTCGGTTTCTTGAAGTACGGGGCCTTCGTCCCTCCTGAGCTCT	2128

Qy	1603	TCGGCTCCGAGTTCTTCATGGGACGGCTGATGAGGAGGATCCCGGAGCCCCGGATCTGCT	1662
Db	2129	TCGGCTCCGAGTTCTTCATGGGACGGCTGATGAGGAGGATCCCGGAGCCCCGGATCTGCT	2188
Qy	1663	TTCTGGAAGCCATCTGGAGCAACATTTTCTCCCTGAACCTGCTGGATGCCTGGTATGACC	1722
Db	2189	TTCTGGAAGCCATCTGGAGCAACATTTTCTCCCTGAACCTGCTGGATGCCTGGTATGACC	2248
Qy	1723	TCACCAGTTCTGGGGAGTCCTGGAACAGCACATCAAGGACAAGACCAGGAGCTTAGAGA	1782
Db	2249	TCACCAGTTCTGGGGAGTCCTGGAACAGCACATCAAGGACAAGACCAGGAGCTTAGAGA	2308
Qy	1783	AGGAGCCCCTGACCACCTCGGGGACCTCCTCGCGGCTGGAGGCCTCGTGGCTGCAGCCAG	1842
Db	2309	AGGAGCCCCTGACCACCTCGGGGACCTCCTCGCGGCTGGAGGCCTCGTGGCTGCAGCCAG	2368
Qy	1843	GCACGGCGCTGGCCCAGGCATTTAAAGGCTTCCTGACAGGCAGGCCCCCTCCACCAGCGCA	1902
Db	2369	GCACGGCGCTGGCCCAGGCATTTAAAGGCTTCCTGACAGGCAGGCCCCCTCCACCAGCGCA	2428
Qy	1903	GCCCCAACTTCCTCCAGGGCCTCCAGCTGCACCAGGACTACTGTAGCCACAAAGACTTCT	1962
Db	2429	GCCCCAACTTCCTCCAGGGCCTCCAGCTGCACCAGGACTACTGTAGCCACAAAGACTTCT	2488
Qy	1963	CCACCTGGGCAGACTACCAGCTTGACTCCATGCCCAGCCAGCTGACCCCCAAGGAGCCCC	2022
Db	2489	CCACCTGGGCAGACTACCAGCTTGACTCCATGCCCAGCCAGCTGACCCCCAAGGAGCCCC	2548
Qy	2023	GGCTCTGCCTGGTGGACGCCGCCTACTTCATCAACACCAGCTCTCCCTCCATGTTCCGGC	2082
Db	2549	GGCTCTGCCTGGTGGACGCCGCCTACTTCATCAACACCAGCTCTCCCTCCATGTTCCGGC	2608
Qy	2083	CAGGCCGAGGCTGGACCTCATCCTCTCCTTCGACTACTCCCTATCTGCGCCCTTCGAGG	2142
Db	2609	CAGGCCGAGGCTGGACCTCATCCTCTCCTTCGACTACTCCCTATCTGCGCCCTTCGAGG	2668
Qy	2143	CACTGCAGCAGACGGAGCTGTACTGCCGGGCCCCGGGGGCTGCCCTTCCCCCGGGTGGAAC	2202
Db	2669	CACTGCAGCAGACGGAGCTGTACTGCCGGGCCCCGGGGGCTGCCCTTCCCCCGGGTGGAAC	2728
Qy	2203	CCAGCCCTCAGGACCAGCACCAGCCAAGGGAATGCCACCTCTTCTCAGACCCCGCCTGCC	2262
Db	2729	CCAGCCCTCAGGACCAGCACCAGCCAAGGGAATGCCACCTCTTCTCAGACCCCGCCTGCC	2788
Qy	2263	CCGAGGCCCGATCCTGCTGCACTTCCCGCTGGTCAATGCCTCCTTCAAGGACCACTCAG	2322
Db	2789	CCGAGGCCCGATCCTGCTGCACTTCCCGCTGGTCAATGCCTCCTTCAAGGACCACTCAG	2848
Qy	2323	CCCCCGGTGTCCAGCGCAGCCCCGAGAGCTCCAGGGTGGCCAAGTGGATCTCACCGGGG	2382
Db	2849	CCCCCGGTGTCCAGCGCAGCCCCGAGAGCTCCAGGGTGGCCAAGTGGATCTCACCGGGG	2908
Qy	2383	CCACCTGCCCCCTACACCCTGTCCAACATGACCTACAAGGAGGAAGACTTCGAGCGCCTGC	2442
Db	2909	CCACCTGCCCCCTACACCCTGTCCAACATGACCTACAAGGAGGAAGACTTCGAGCGCCTGC	2968
Qy	2443	TGCGGCTCAGTGACTACAACGTGCAGACCAGCCAGGGTGCCATCCTGCAGGCCCTGAGGA	2502
Db	2969	TGCGGCTCAGTGACTACAACGTGCAGACCAGCCAGGGTGCCATCCTGCAGGCCCTGAGGA	3028
Qy	2503	CCGCGCTGAAGCACCGGACTCTAGAGGCGAGGCCTCCAAGGGCACAGACCTGAGGTTGCT	2562

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Db      3029 CCGCGCTGAAGCACCGGACTCTAGAGGCGAGGCCTCCAAGGGCACAGACCTGAGGTTGCT 3088
      |||
Qy      2563 CAGAGGCTGCAGGACCCTCCAGGGCCTGCGGGCATAACCTGATCTGTAGCTGGGCTCAGC 2622
      |||
Db      3089 CAGAGGCTGCAGGACCCTCCAGGGCCTGCGGGCATAACCTGATCTGTAGCTGGGCTCAGC 3148
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Qy      2623 CACAGGCCTTCCTGGTTGGAGTTCTGGGCTCTCCCAGGCCTGGGTGGCC 2671
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Db      3149 CACAGGCCTTCCTGGTTGGAGTTCTGGGCTCTCCCAGGCCTGGGTGGCC 3197

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